

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/720,896B
Source: 1FW16
Date Processed by STIC: 6/21/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/720,896B

TIME: 15:21:32

Input Set : A:\67452507.APP

Output Set: N:\CRF4\06212006\J720896B.raw

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3 <110> APPLICANT: SOLARI, ROBERTO CELESTE ERCOLE
4     CHAMPION, BRIAN ROBERT
5     WARD, GEORGE ALBERT
7 <120> TITLE OF INVENTION: CONJUGATE OF A TRANSPORT PROTEIN AND A PROTEIN FOR
8     MODULATION OF NOTCH SIGNALLING
10 <130> FILE REFERENCE: 674525-2007
12 <140> CURRENT APPLICATION NUMBER: 10/720,896B
13 <141> CURRENT FILING DATE: 2003-11-24
15 <150> PRIOR APPLICATION NUMBER: PCT/GB02/02438
16 <151> PRIOR FILING DATE: 2002-05-24
18 <150> PRIOR APPLICATION NUMBER: GB 0112818.0
19 <151> PRIOR FILING DATE: 2001-05-25
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: PatentIn Ver. 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR primer
32     for amplifying HES1 promoter from mouse genomic DNA
34 <400> SEQUENCE: 1
35 ggggtaccct caggcgcgcg ccattggcc 29
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 29
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR primer
45     for amplifying HES1 promoter from mouse genomic DNA
47 <400> SEQUENCE: 2
48 gaagatctgc ttacgtcctt ttacttgac 29
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 26
53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
58     major late promoter TATA-box motif with BglIII and HindIII
59     cohesive ends
61 <400> SEQUENCE: 3
62 gatctggggg gctataaaag ggggta 26
65 <210> SEQ ID NO: 4

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66 <211> LENGTH: 26
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Adenovirus
72     major late promoter TATA-box motif with BglII and HindIII
73     cohesive ends
75 <400> SEQUENCE: 4
76 agcttaccgcc cttttatagc ccccca                26
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 61
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic CBF-1
86     promoter tetramer with XhoI and BglII cohesive ends
88 <400> SEQUENCE: 5
89 tcgagaccgt ggggaacttaa ccgtgggaac ttaaccgtgg gaacttaacc gtgggaactt 60
90 a                                           61
93 <210> SEQ ID NO: 6
94 <211> LENGTH: 61
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic CBF-1
100     promoter tetramer with XhoI and BglII cohesive ends
102 <400> SEQUENCE: 6
103 gatctaagtt cccacggtta agttcccacg gttaagttcc cacggttaag ttcccacggt 60
104 c                                           61
107 <210> SEQ ID NO: 7
108 <211> LENGTH: 39
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
114     amplicon for generating a truncated fragment of
115     human Notch1 cDNA
118 <400> SEQUENCE: 7
119 aaaggatcca ccatggcacg caagcgccgg cgcagtcac                39
122 <210> SEQ ID NO: 8
123 <211> LENGTH: 31
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PCR
129     amplicon for generating a truncated fragment of
130     human Notch1 cDNA
132 <400> SEQUENCE: 8
133 gcgcctcgag ttagtcacg ggcgagagca t                31

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136 <210> SEQ ID NO: 9
137 <211> LENGTH: 91
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligo
143     annealed to the NIC2202 sequence to remove the stop codon
144     from theNIC2202 fragment of human Notch1 cDNA
146 <400> SEQUENCE: 9
147 cctggcctgt ggaagcaagg aggccaagga cctcaaggca cggaggaaga agtcccagga 60
148 tggcaagggc tgctgtctgg acggcgccg c                               91
151 <210> SEQ ID NO: 10
152 <211> LENGTH: 95
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Oligo
158     annealed to the NIC2202 sequence to remove the stop codon
159     from theNIC2202 fragment of human Notch1 cDNA
161 <400> SEQUENCE: 10
162 tcgagcggcc gccgtccagc aggcagccct tgccatcctg ggactttcttc ctccgtgcct 60
163 tgaggtcctt ggctccttg cttccacagg ccagg                               95
166 <210> SEQ ID NO: 11
167 <211> LENGTH: 2556
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <220> FEATURE:
172 <221> NAME/KEY: MOD_RES
173 <222> LOCATION: (891)
174 <223> OTHER INFORMATION: Variable amino acid
176 <400> SEQUENCE: 11
177 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
178   1           5           10           15
180 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
181           20           25           30
183 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
184           35           40           45
186 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
187           50           55           60
189 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
190   65           70           75           80
192 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
193           85           90           95
195 Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
196           100          105          110
198 Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
199           115          120          125
201 Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys
202   130          135          140

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204 Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala
205 145 150 155 160
207 Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg
208 165 170 175
210 Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly
211 180 185 190
213 Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala
214 195 200 205
216 Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro
217 210 215 220
219 Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr
220 225 230 235 240
222 His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu
223 245 250 255
225 Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys
226 260 265 270
228 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr
229 275 280 285
231 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn
232 290 295 300
234 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn
235 305 310 315 320
237 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile
238 325 330 335
240 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp
241 340 345 350
243 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
244 355 360 365
246 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
247 370 375 380
249 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
250 385 390 395 400
252 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
253 405 410 415
255 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
256 420 425 430
258 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
259 435 440 445
261 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
262 450 455 460
264 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
265 465 470 475 480
267 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
268 485 490 495
270 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
271 500 505 510
273 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
274 515 520 525
276 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu

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277      530      535      540
279 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly
280 545      550      555      560
282 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His
283      565      570      575
285 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg
286      580      585      590
288 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser
289      595      600      605
291 Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala
292      610      615      620
294 Tyr Leu Cys Phe Cys Leu Lys Gly Thr Thr Gly Pro Asn Cys Glu Ile
295 625      630      635      640
297 Asn Leu Asp Asp Cys Ala Ser Ser Pro Cys Asp Ser Gly Thr Cys Leu
298      645      650      655
300 Asp Lys Ile Asp Gly Tyr Glu Cys Ala Cys Glu Pro Gly Tyr Thr Gly
301      660      665      670
303 Ser Met Cys Asn Ser Asn Ile Asp Glu Cys Ala Gly Asn Pro Cys His
304      675      680      685
306 Asn Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly Phe Thr Cys Arg Cys
307      690      695      700
309 Pro Glu Gly Tyr His Asp Pro Thr Cys Leu Ser Glu Val Asn Glu Cys
310 705      710      715      720
312 Asn Ser Asn Pro Cys Val His Gly Ala Cys Arg Asp Ser Leu Asn Gly
313      725      730      735
315 Tyr Lys Cys Asp Cys Asp Pro Gly Trp Ser Gly Thr Asn Cys Asp Ile
316      740      745      750
318 Asn Asn Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Gly Thr Cys
319      755      760      765
321 Lys Asp Met Thr Ser Gly Ile Val Cys Thr Cys Arg Glu Gly Phe Ser
322      770      775      780
324 Gly Pro Asn Cys Gln Thr Asn Ile Asn Glu Cys Ala Ser Asn Pro Cys
325 785      790      795      800
327 Leu Asn Lys Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn
328      805      810      815
330 Cys Leu Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro
331      820      825      830
333 Cys Ala Pro Ser Pro Cys Arg Asn Gly Gly Glu Cys Arg Gln Ser Glu
334      835      840      845
336 Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly
337      850      855      860
339 Gln Thr Cys Glu Val Asp Ile Asn Glu Cys Val Leu Ser Pro Cys Arg
340 865      870      875      880
W--> 342 His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys
343      885      890      895
345 Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys
346      900      905      910
348 Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn
349      915      920      925

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/21/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 891

VERIFICATION SUMMARY

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Input Set : A:\67452507.APP

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L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:880